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FIG. 1.

JDF-3 DNA polymerase nucleotide sequence: 2331 nucleotides (SEQ ID NO: 1)

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGG  
CGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCTACGCGCTCCTCAGGGACGACTCTGCCA  
TCGAAGAAATCAAAAAGATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTG  
AAGAAAAAGTTCTCTCGGCAGGTCTGTGGAGGTCTGGGTCTCTACTTCACGCACCCGCAGGACGTTCCGGC  
AATCCGCGACAAAATAAGGAAGCACCCCGCGTCATCGACATCTACGAGTACGACATACCCTTCGCCAAGC  
GCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCCTTCGACATC  
GAGACGCTCTACCACGAGGGAGAAGAGTTTGGAAACCGGGCCGATTCTGATGATAAGCTACGCCGATGAAAG  
CGAGGCGCGCGTGATAACCTGGAAGAAGATCGACCTTCCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGA  
TGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATAACGGCGACAAC  
TTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTTACCCTCGGGAGGGACGGGAG  
CGAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTCGACCTTT  
ATCCAGTCATAAGGCGCACCATAAACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTTCGGC  
AAGCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGGCAGGGGCTTGAGAGGGT  
CGCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCC  
AGCTTTCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCCCGCTCCAGCACCGGCAACCTCGTCGAGTGG  
TTCTCCTAAGGAAGGCCCTACGAGAGGAACGAACCTCGCTCCCAACAAGCCCGACGAGAGGGAGCTGGCGAG  
GAGAAGGGGGGGCTACgCGGTGGCTACGTCAAGGAGCCGGAGCGGGGACTGTGGGACAATATCGTGATC  
TAGACTTTCGTAGTCTCTACCCCTCAATCATAATCACCCACAACGTCTCGCCAGATACGCTCAACCGCGAG  
GGGTGTAGGAGCTACGACGTTGCCCCCGAGGTGCGTCACAAGTTCTGCAAGGACTTCCCCGGCTTCATTCC  
GAGCCTGCTCGGAAACCTGCTGGAGGAAAGGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGC  
TGGAGAAGAATCTCCTCGATTACAGGCAACGCGCCATCAAGATTCTCGCCAACAGCTACTACGGCTACTAC  
GGCTATGCCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACAT  
CGAAATGGTCATCAGAGAGCTTGAGGAAAAGTTGCGTTTTTAAAGTCCTCTATGCAGACACAGACGGTCTCC  
ATGCCACCATTCTTGGAGCGGACGCTGAAACAGTCAAGAAAAGGCAATGGAGTTCTTAAACTATATCAAT  
CCCAAAGTGGCCGGCCTTCTCGAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAA  
AAAGTACGCGGTATCGACGAGGAGGGCAAGATAACCACGCGCGGGCTTGAGATAGTCAGGCGCGACTGGA  
GCGAGATAGCGAAGGAGACGCAGGCGAGGGTTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCC  
GTCAGAATTGTGAGGGAAGTCACCGAAAAGCTGAGCAAGTACGAGGTTCCGCCCGGAGAAGCTGGTTATCCA  
CGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGGCCGCACGTAGCCATAGCGAAGcGTTTGG  
CCGCCAGAGGTGTTAAAATCCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATA  
GGCGACAGGGCGATTCCCTTCGACGAGTTCGACCCGACGAAGCACAAAGTACGATGCGGACTACTACATCGA  
GAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACC  
AGAAGACGAGGCAGGTCTGGGCTTGGCGCGTGGCTGAAGCCGAAGGGGAAGAAGAAGTGA

FIG. 2.  
JDF-3 DNA polymerase amino acid sequence (SEQ ID NO: 2)  
Theoretical molecular weight: 90.3 kD

MILDVDYITENGKPVIRVFKKENGEFRIEYDREFEPYFYALLRDDS AIEEIKKITAERHGRVVKVKRAEKV  
KKKFLGRSVEVWVLYFTHPQDVPAIRDKIRKHPAVIDIYDYDIPFAKRYLIDKGLIPMEGEEELKILMSFDI  
ETLYHEGEEFGTGPILMISYADESEARVITWKKIDLPYVEVVSTEKEMIKRFLRVVKEKDPDVLITYNGDN  
FDFAYLKKRCEKLGVSFTLGRDGSEPKIQRMGDRFAVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFG  
KPKEKVYAEIATAWETGEGLERVARYSMEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSTGNLVEW  
FLLRKAYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNRE  
GCRSYDVAPEVGHKFCDFPGFIPSLGNNLEERQKIKRKMATLDPLEKNLLDYRQRAIKILANSYYGY  
GYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHATIPGADAETVKKKAMEFLNYIN  
PKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEA  
VRIVREVTEKLSKYEVPPEKLVIHEQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYIVLKGSGRI  
GDRAIPFDEFDPTKHKYDADYYIENQVLPAPERILRAFGYRKEDLRYQKTRQVGLGAWLKPKGKKK

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FIG. 3.

JDF-3 DNA polymerase with intein sequence (SEQ ID NO: 3)

MILDVDYITENGKPVIRVFKKENGEFRIEYDREFEPYFYALLRDDS AIEE  
 IKKITAERHGRVVKVKRAEKVKKKFLGRSVEVWVLYFTHPQDVPAIRDKI  
 RKHPAVIDIYEDIPFAKRYLIDKGLIPMEGEEELKMSFDIETLYHEGE  
 EFGTGPILMISYADESEARVITWKKIDLPYVEVVSTEKEMIKRFLRVVKE  
 KDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGRDGSSEPKIQRMGDRFAV  
 EVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKKVKYAEIATAWE  
 TGEGLERVARYSMEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSSSTG  
 NLVEWFLLRKAYERNELAPNKPDERELARRRGGYAGGYVKEPERGLWDNI  
 VYLDFRSLYPSIIITHNVSPDTLNRGCRSYDVAPEVGHKFKCDFPGFIP  
 SLLGNLLEERQKIKRKMATLDPLEKNLLDYRQRAIKILAN

Extein 1

SLLPGEWVA  
 VIEGGKLRPVIRIGELVDGLMEASGERVKRDGDTEVLEVEGLYASPSSTGSP  
 RKPAQCR\*KP\*\*GTAMPGKFTE\*LSTPEGGLSVTRGHSLFAYRDASLWR\*  
 RGRRRFKPGDLLAVPSG\*PSRRGGRGSTSLNCSSNCPRRKRPTCHRHSGK  
 GRKNFFRGMLRTLRLWIFGEEKTGGRPGATWSTLRGLGYVKLRKIGYGVVD  
 REGLGKVPRFYERLVEVIRYNGNRGEFIADFNALRPVLRMMPEKELEEW  
 LVGTRNGFRIRPFIEVDWKFAKLLGYVSEGSAGKWKNTGGWSYSVRLY  
 NEDGSVLDDMERLARSSLGA\*ARGELRRDFKEDGLHNLRGALRFTGREQE  
 GSVAYLHVP\*GGPLGLP\*GVLHRRRRRSPEQDGSALHQERASG\*RPRPAP  
 ELAGRLSDKRPPRQRLQGLRERGTALYRVPEAEERLTYSHVIPREVLEE  
 TSAGPSRRT\*VTGNSGSWWKAGSSTRKGPVG\*AGSSTGI\*SSTGSRKSGR  
 KATRGTTST\*ALRRTRTSAGGLWVPLRAQX

Intein 1

SYGGYGYARARWYCRECAES  
 VTAWGREYIEMVIRELEEKFGFKVLYADTDGLHATIPGADAETVKKKAME  
 FLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVR  
 RDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKLVI  
 HEQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYIVLKGSGRIGD  
 RAIPFDEFDPTKHKYDADYYIENQVLPAVERILRAFGYRKEDLRYQKTRQ  
 VGLGAWLKPKGKKK

Extein 2

FIG. 4.  
JDF-3 DNA polymerase genomic sequence (SEQ ID NO: 4)

AATTCCACTGCCGTGTTTAACCTTTCCACCGTTGAACTTGAGGGTGATTT  
TCTGAGCCTCCTCAATCACTTAATCGAGACCGCGGATTACCTTGAACTGG  
TACACGTTCAACGATTTCGGTTCCTTGTAAATGGTCGATACTGGGCCGTGCTG  
GATTTTCTAAACGTCTCAAGAACGGCTTTTCATCAACGGAACTGCCACGT 5' untranslated sequence  
CTCCGCCGTCTGAGGGTTAAACCTGAAGTTCAAGACTTTGCAACGGAAT  
GGCGAGAGAACGGCGACTACCCAGTGAAGAGCTTTTGAAAGCCAAAGC  
CGAGCTTCAGCGAATGTGCGGTGCCCTTGTTCAGAGTTGTGAGCCCTTG  
ATTGTTGTTTTCTCCTCTTTTCTGATAACATCGATGGCGAAGTTTATTAG  
TTCTCAGTTCGATAATCAGGCAGGTGTTGGTC

ATGATCCTTGACGTTGAT  
TACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAA  
CGGCGAGTTTCAAGATTGAATACGACCGCGAGTTCGAGCCCTACTTCTACG  
CGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCG  
GAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAGAA  
AAAGTTCCTCGGCAGGTCTGTGGAGGTCTGGGTCTCTACTTCACGCACC  
CGCAGGACGTTCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGCGGTCT  
ATCGACATCTACGAGTACGACATAACCTTCGCCAAGCGCTACCTCATAGA  
CAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAACTCATGTCCT  
TCGACATCGAGACGCTCTACCACGAGGGAGAAGAGTTTGGAAACCGGGCCG  
ATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGCGTGATAACCTG  
GAAGAAGATCGACCTTCTTACGTTGAGGTGTCTCCACCGAGAAGGAGA  
TGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTG  
ATAACATACAACGGCGACAACCTTCGACTTCGCCTACCTGAAAAAGCGCTG  
TGAGAAGCTTGGCGTGAGCTTTACCTTCGGGAGGGACGGGAGCGAGCCGA Extein 1  
AGATACAGCGCATGGGGGACAGGTTTTCGGGTTCGAGGTGAAGGGCAGGGTA  
CACTTCGACCTTTATCCAGTCATAAGGCGCACCATAAACCTCCCGACCTA  
CACCCCTTGAGGCTGTATACGAGGCGGTTTTTCGGCAAGCCCAAGGAGAAGG  
TCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGCTTGAG  
AGGGTCGCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGG  
CAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCAGGGCTCATCGGCCAAG  
GCCTCTGGGACGTTTCCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTC  
CTCCTAAGGAAGGCCTACGAGAGGAACGAACCTCGCTCCCAACAAGCCCGA  
CGAGAGGGAGCTGGCGAGGAGAAGGGGGGGCTACGCCGTTGGCTACGTCA  
AGGAGCCGGAGCGGGGACTGTGGGACAATATCGTGTATCTAGACTTTCGT  
AGTCTCTACCTTCAATCATAATCACCCACAACGTCTCGCCAGATACGCT  
CAACCGCGAGGGGTGTAGGAGCTACGACGTTGCCCGGAGGTTCGGTCACA  
AGTTCTGCAAGGACTTCCCGGCTTCATTCCGAGCCTGCTCGGAAACCTG  
CTGGAGGAAAGGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCC  
GCTGGAGAAGAATCTCCTCGATTACAGGCAACGCGCCATCAAGATTCTCG  
CCAAC

AGCCTTCTTCCCGGGGAGTGGGTTGCGGTTCATTGAAGGGGGGAAA  
CTCAGGCCCGTCCGCATCGGCGAGCTGGTTGATGGACTGATGGAAGCCAG  
CGGGGAGAGGGTGAAGAGACGGCGACACCGAGGTCCTTGAAGTCGAGG  
GGCTTTACGCCTCTCCTTCGACAGGGAGTCCAAGAAAGCCCGCACAAATGC  
CGGTGAAAGCCGTGATAAGGCACCGCTATGCCGGGGAAGTTTACAGAATA  
GCTCTCAACTCCGGAAGGAGGATTAAGCGTGACGCGCGGCCACAGCCTCT  
TCGCGTACCGGGACGCGAGCTTGTGGAGGTGACGGGGAGGAGGAGGTTTC  
AAGCCCGGCGACCTCCTGGCGGTGCCAAGCGGATAACCCTCCCGGAGAGG  
Intein 1

AGGGAGAGGCTCAACATCGTTGAACTGCTCCTCGAACTGCCCCGAGGAGGA  
AACGGCCGACATGTCATCGACATTCCGGCAAGGGTAGAAAGAACTTCTTC  
AGGGGAATGCTCAGAACCCCTCCGCTGGATTTTCGGGGAGGAGAAGACCGG Intein 1  
AGGGCGGCCAGGCGCTACCTGGAGCACCTTGCGTGGGCTCGGCTACGTGA  
AGCTGAGGAAAATCGGCTACGGGGTGGTTGATAGGGAGGACTGGGAAAG  
GTACCGCGCTTCTACGAGAGGCTCGTGGAGGTAATCCGCTACAACGGCAA  
CAGGGGGGAGTTCATCGCCGATTTCAACGCGCTCCGCCCCGTCTCCGCC  
TGATGATGCCCCGAGAAGGAGCTTGAAGAGTGGCTCGTTGGGACGAGGAAC  
GGGTTTCAAGATAAGGCCGTTTATAGAGGTTGATTGGAAGTTTCGCAAAGCT  
CCTCGGCTACTACGTGAGCGAGGGGAGCGCCGGGAAGTGGAAAAACCGGA  
CCGGGGGCTGGAGCTACTCGGTGAGGCTTTACAACGAGGACGGGAGCGTT  
CTCGACGACATGGAGAGACTCGCGAGGAGTTCTTTGGGGGCGTGAGCGCG  
GGGGGAACACGTGAGATTTCAAAGAAGATGGCCTACATAATCTTCGAG  
GGGCTCTGCGGTTACCGGCCGAGAACAGAGGGTTCCGTGGCTTATCTT  
CACGTCCCCTGAGGAGGTCCGCTGGGCCTTCTTGAGGGGTACTTCATCG  
GCGACGGCGACGTTACCCGAGCAAGATGGTTCGGCTCTCCACCAAGAGC  
GAGCTTCTGGCTAACGGCCTCGTCTGCTCCTGAACTCGCTGGGCGTCTC  
AGCGATAAACGTCCGCCACGACAGCGGGGTTTACAGGGTCTACGTGAACG  
AGGAAGTGCCTTTTACAGAGTACCGGAAGCGGAAGAAGCCTCACTTACT  
CCCACGTACATCCGAGGGAAGTGCTGGAGGAGACTTCGGCCGGGCCTTCC  
AGAAGAACATGAGTCACGGGAAATTCAGGGAGCTGGTGGAAAGCGGGGAG  
CTCGACGGCGAAAGGGCCGGTAGGATAGGCTGGCTCCTCGACGGGGATAT  
AGTCTCGACAGGGTCTCGGAAGTCAGGAAGGAAAGCTACGAGGGGTACG  
TCTACGACCTGAGCGTTGAGGAGGACGAGAACTTCTGGCGGGCTTTGGGT  
TCCTCTACGCGCACAAACNN

AGCTACTACGGCTACTACGGCTATGCCAGGG  
CAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGG  
GAGTACATCGAAATGGTCATCAGAGAGCTTGAGGAAAAGTTCCGTTTAA  
AGTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCTGGAGCGG  
ACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAAT  
CCCAAAGTGCCTCGGCTTCTCGAACTCGAATACGAGGGCTTCTACGTCAG  
GGGCTTCTTCGTACGAAAGAAAAAGTACGCGGTATCGACGAGGAGGGCA  
AGATAACCACGCGCGGGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATA  
GCGAAGGAGACGCGAGGCGAGGGTTTTGGAGGCGATACTCAGGCACGGTGA Extein 2  
CGTTGAAGAGGCCGTGAGAAATGTCAGGGAAGTACCGAAAAGCTGAGCA  
AGTACGAGGTTCCGCCGAGAGAGTGGTTATCCACGAGCAGATAACGCGC  
GAGCTCAAGGACTACAAGGCCACCGCCCGCACGTAGCCATAGCGAAGCG  
TTTGGCCGCCAGAGGTGTTAAAATCCGGCCCGGAAGTGTGATAAGCTACA  
TCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGAC  
GAGTTCGACCCGACGAAGCACAAAGTACGATGCGGACTACTACATCGAGAA  
CCAGGTTCTGCCGCGAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCA  
AGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTGGGCTTGGCGCGTGG  
CTGAAGCCGAAGGGGAAGAAGAAGTGA

GGAATTATCTGGTTTCTTTTCCC  
AGCATTAATGCTTCCGACATTGCCTTATTTATGAACTCCTGTTGTGCC  
TGAGTTTGTGCCAGAAAACAGCCTGTTCTGACGGCGCTTTTCTTGCCAG  
GTCTCTTGAGTTTCGCAAGGGTCTTCTCGACCAGCTCAATGGTCTTGTCTG  
TCATTGTTTNNNNNNNNNNNNNNNNNNNNNNCCGGGGACTTCATACTGGC  
GGTAATAGACAGGGATTCTTCTCAAGGACTTCCCGGGAGGCATTGGAG  
TTTTTTGGTGGGGCTTTACAGGATTGCTCATCTTGTGGATTTCTCGTT  
CGATTGAATCTGTCCACTTGAGGGTGTAGGTGAGACGGTGGAGCGCGTA

TTCCGGGAGCGGGTCTTGAGGCTCCATTTTTCAGTCCTCCTCCGGCGAAG 3' Untranslated sequence  
AAGTGGAAGTCAAGCCGGGTGTTAGCTTATGTTATGTTCCCAACTCCTCC  
AGCACCTCCAGGATCCCCCTCAATCCCGGAACCTCGAAGCCCCCTCTCGTGG  
ATCTTTCTAACTTCCTCTGCCTCCGGGTTTATCCAGACCGCCACATGCC  
GGCTCTCAGCGCACCCCTCGAAATCCTCCGCGTAGGTGTCGCCGATGTGGA  
TTGCCTCGTCCGGCTCGACCCCGAAGCATCGAGCGGTTTTCTGAACATCT  
CGGGCATCGGCTTATACGCCAGAACCTCGTCGGCGAAGAAGGTTCCCTCA  
ATGTAGTCCATCAGGCCGAACCTCTCGAGGGGGGGCCCGGTACCCAATTC  
GCCCTATAGTGAGTCGATTACAATTCACTGGCCGTCGTTTTACAACGTCG  
TGACTGGGAAAACCTGGCGTTACCCAACCTTAAGTCGCTTTGCAGCACAT  
CCCCC

# Preliminary Qualification of Mutants

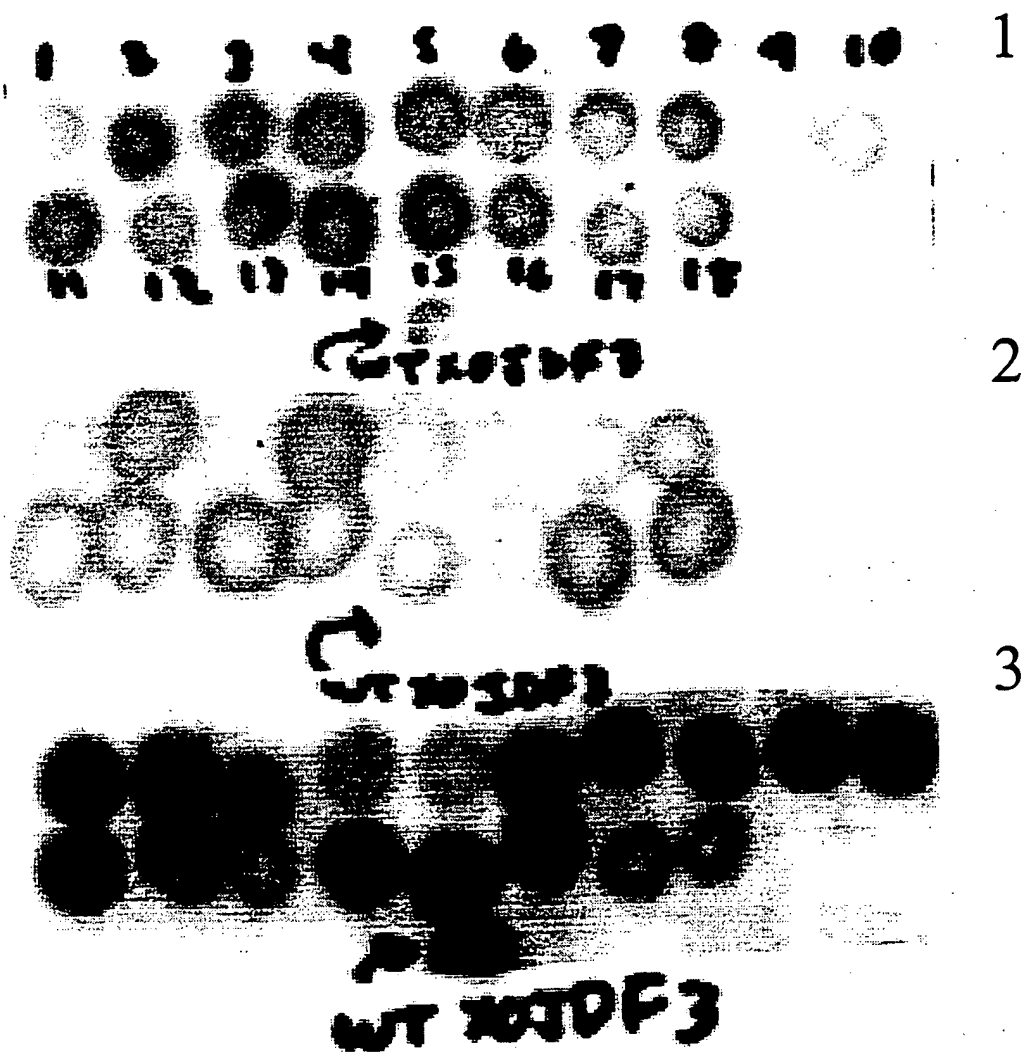


Figure 5



## Sequencing with Purified Mutants

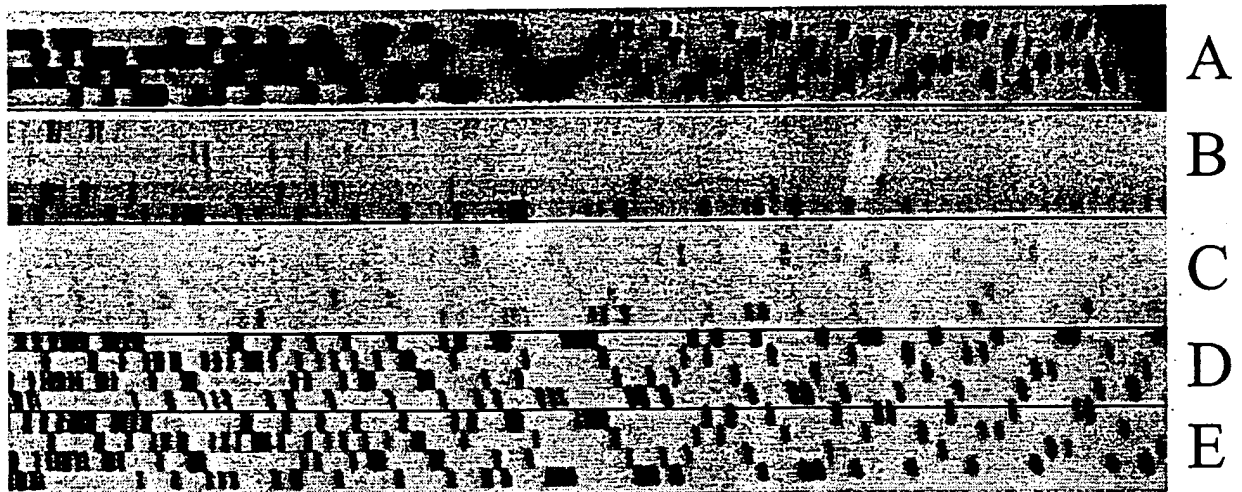


Figure 6

# Sequencing with Dye-labeled Dideoxynucleotides

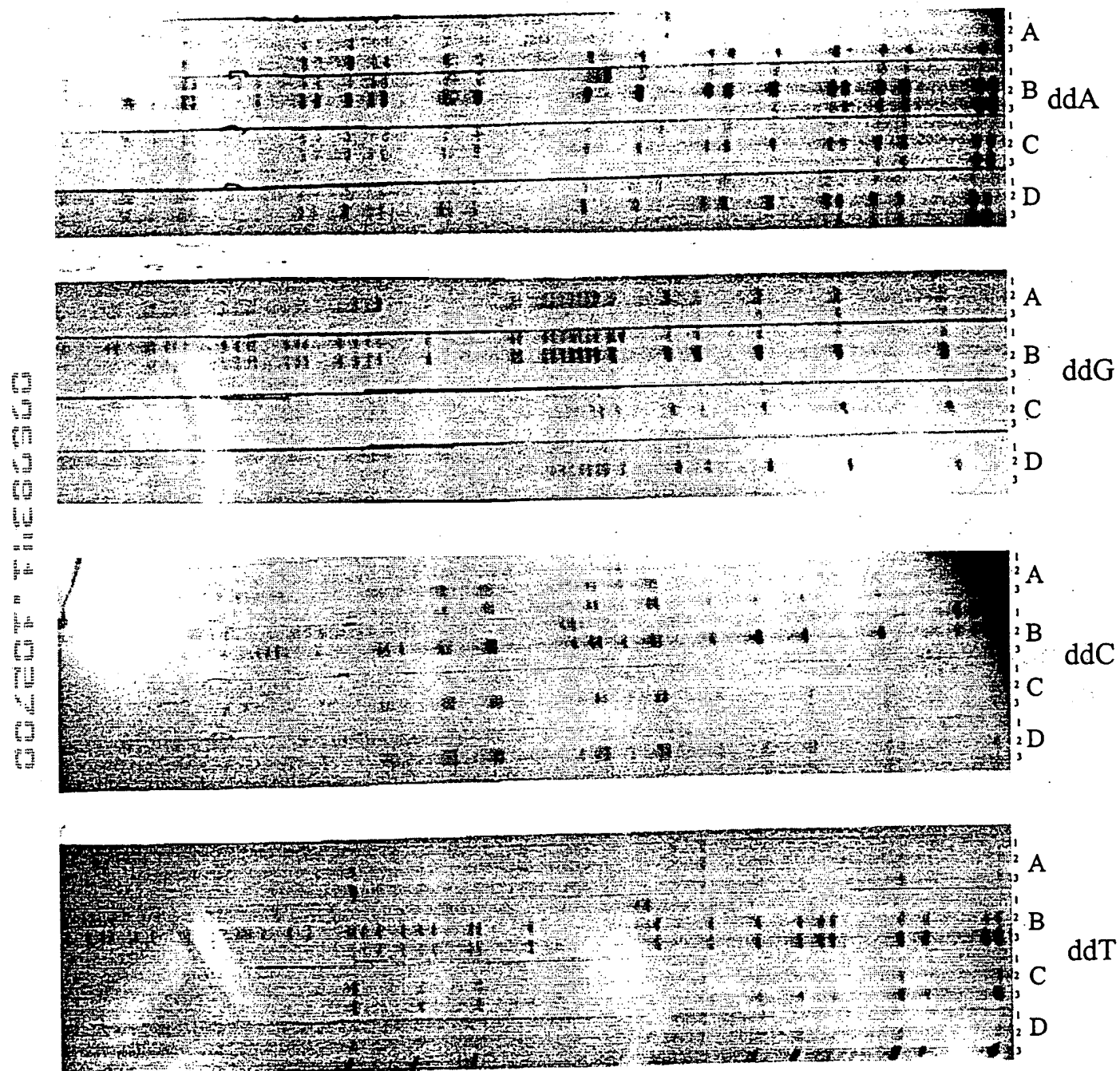


Figure 7

Sequencing with the P410L, A485T Double Mutant  
and  $\alpha$ - $^{33}\text{P}$  Dideoxynucleotides

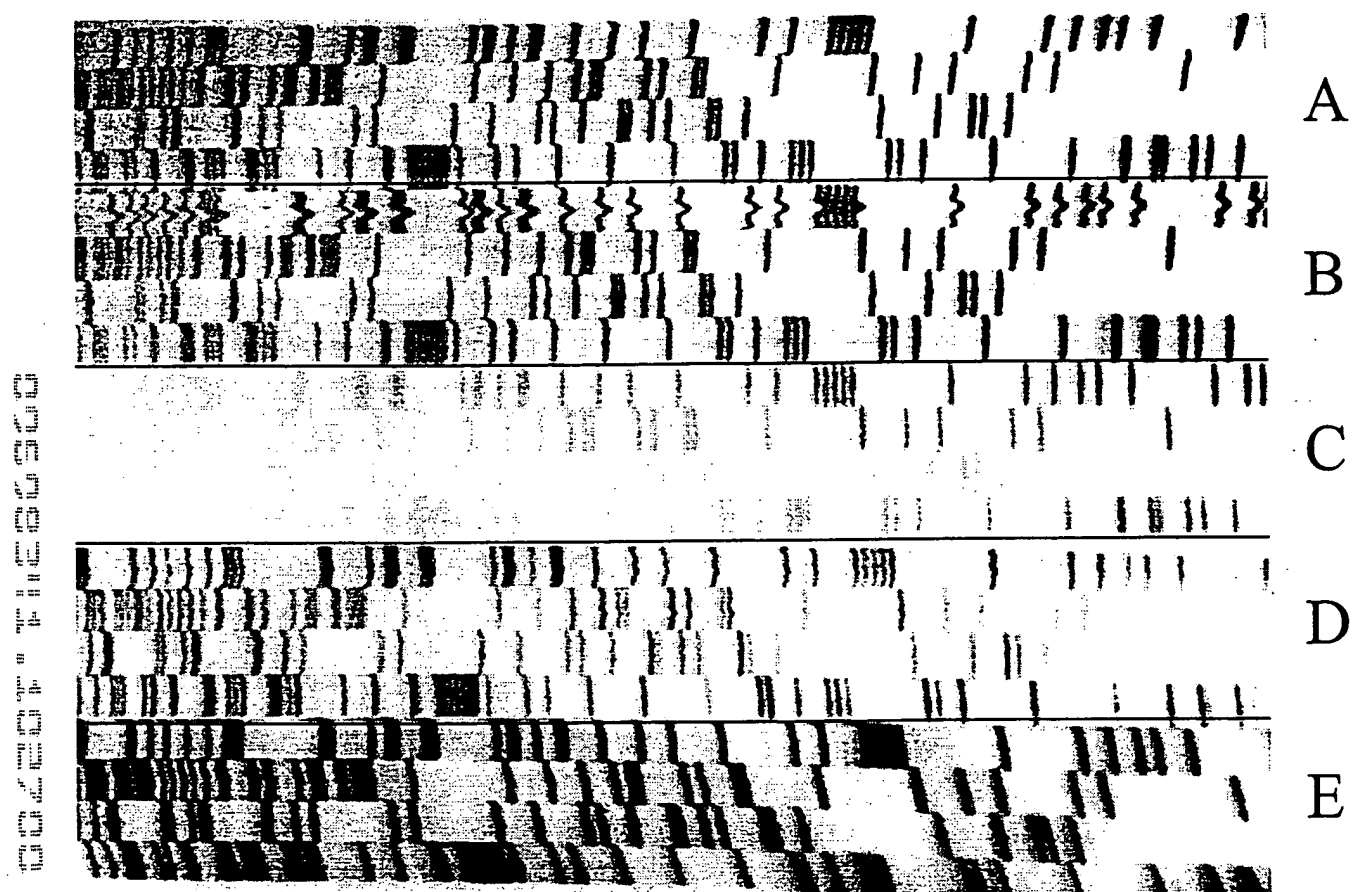
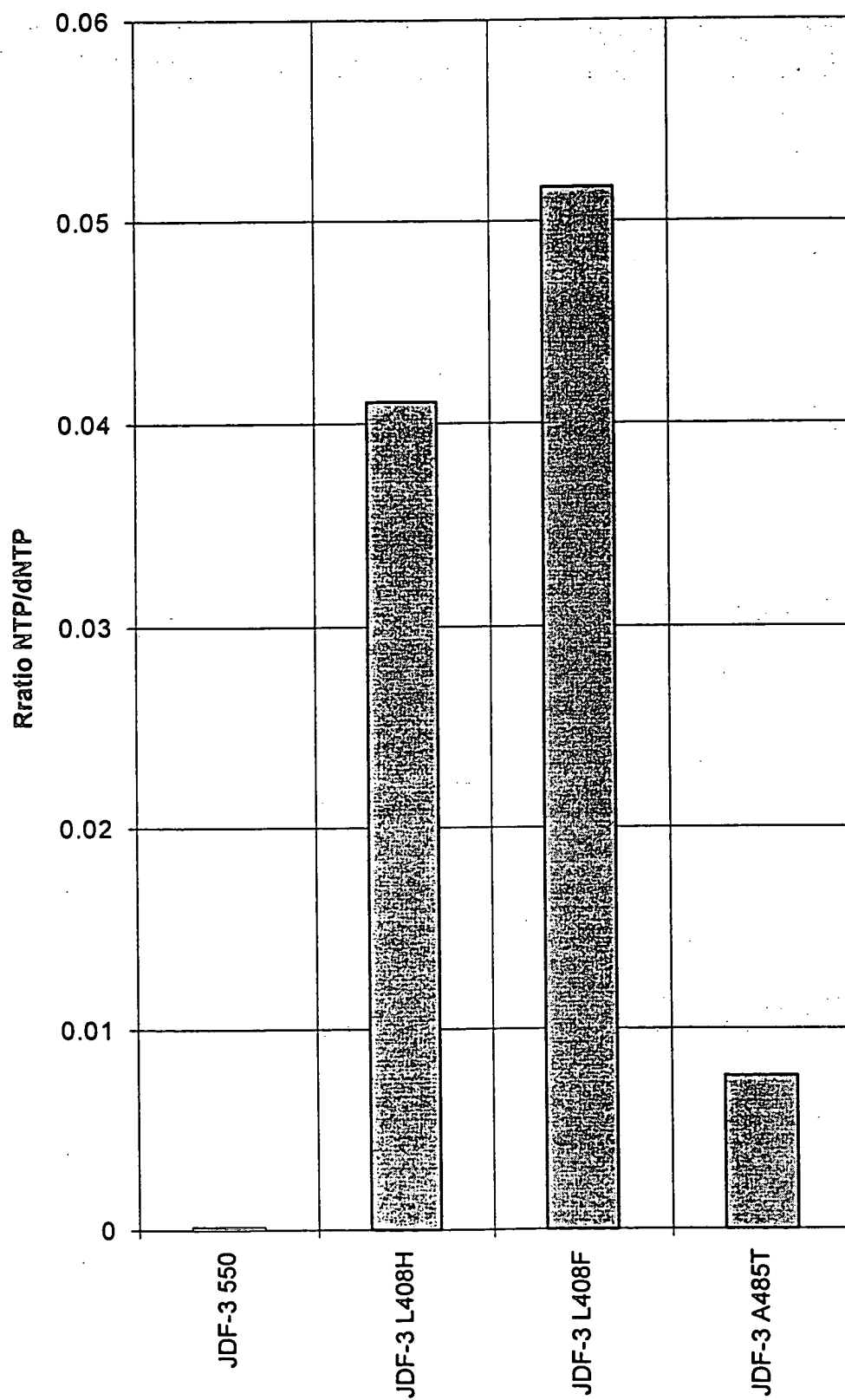


Figure 8

Figure 9



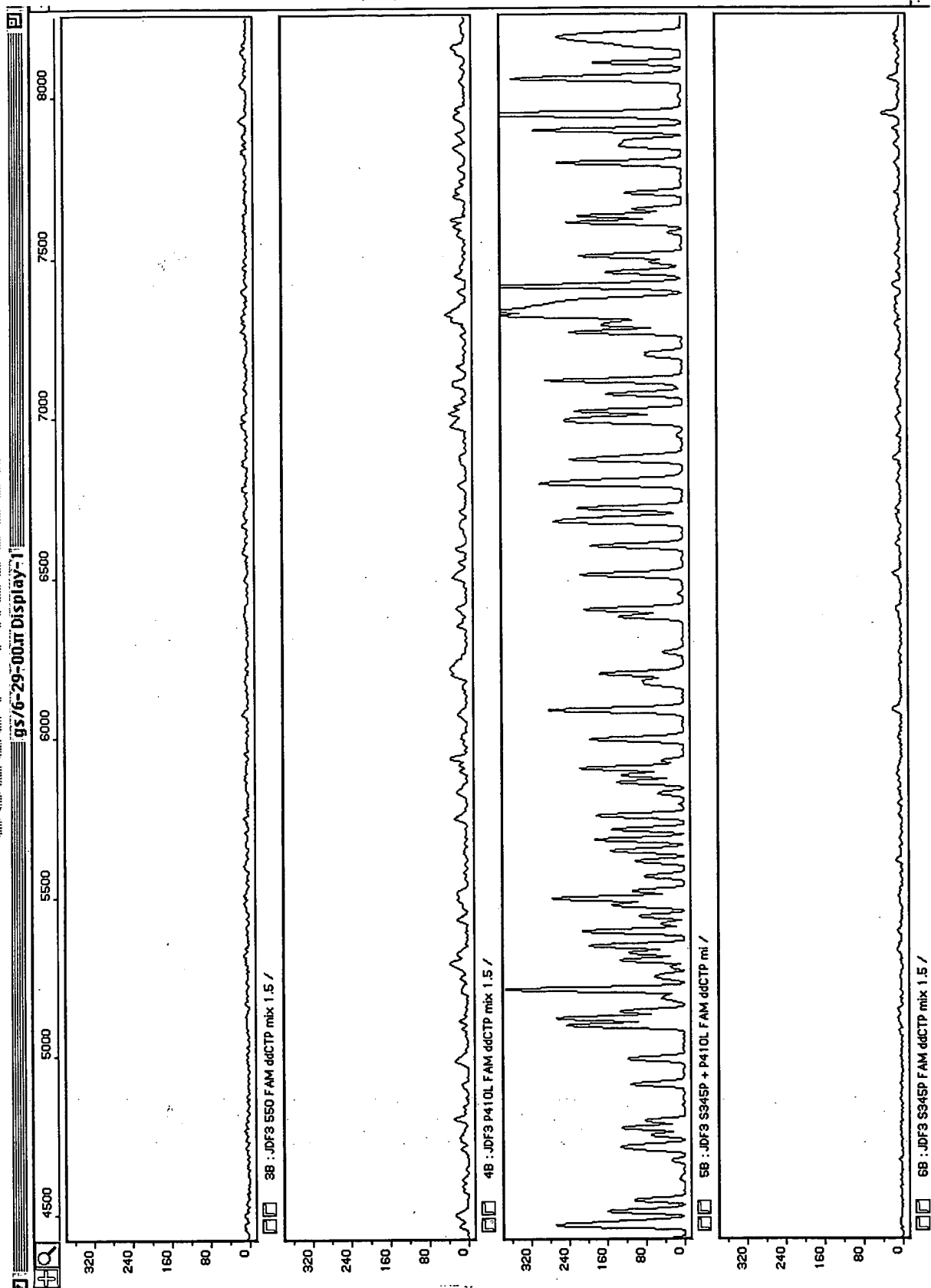


Figure 10

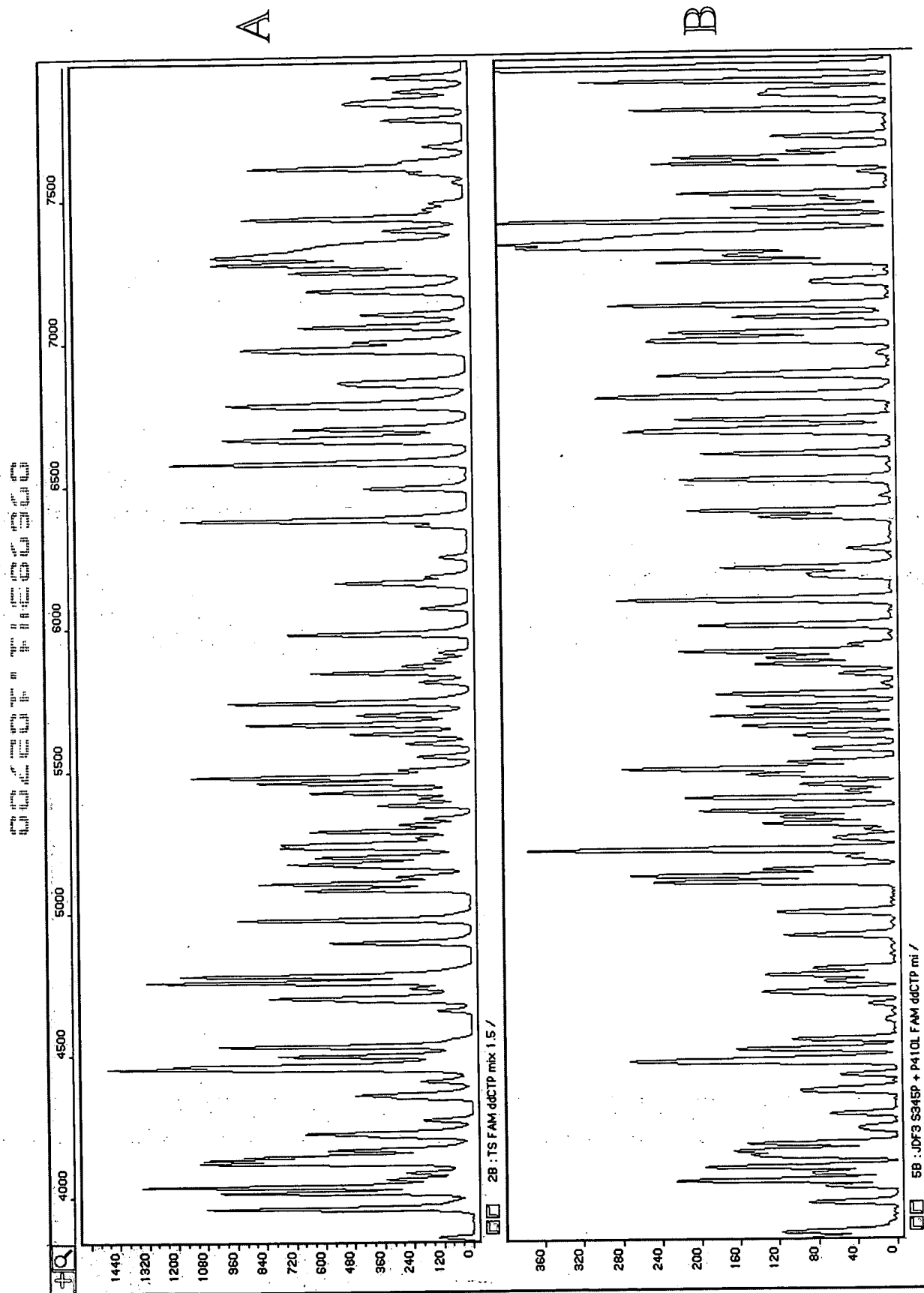


Figure 11

$^{33}\text{P}$  - TAACGTTGGGGGGGGGGCA →  
 TGCAACCCCCCCCCCGTAT

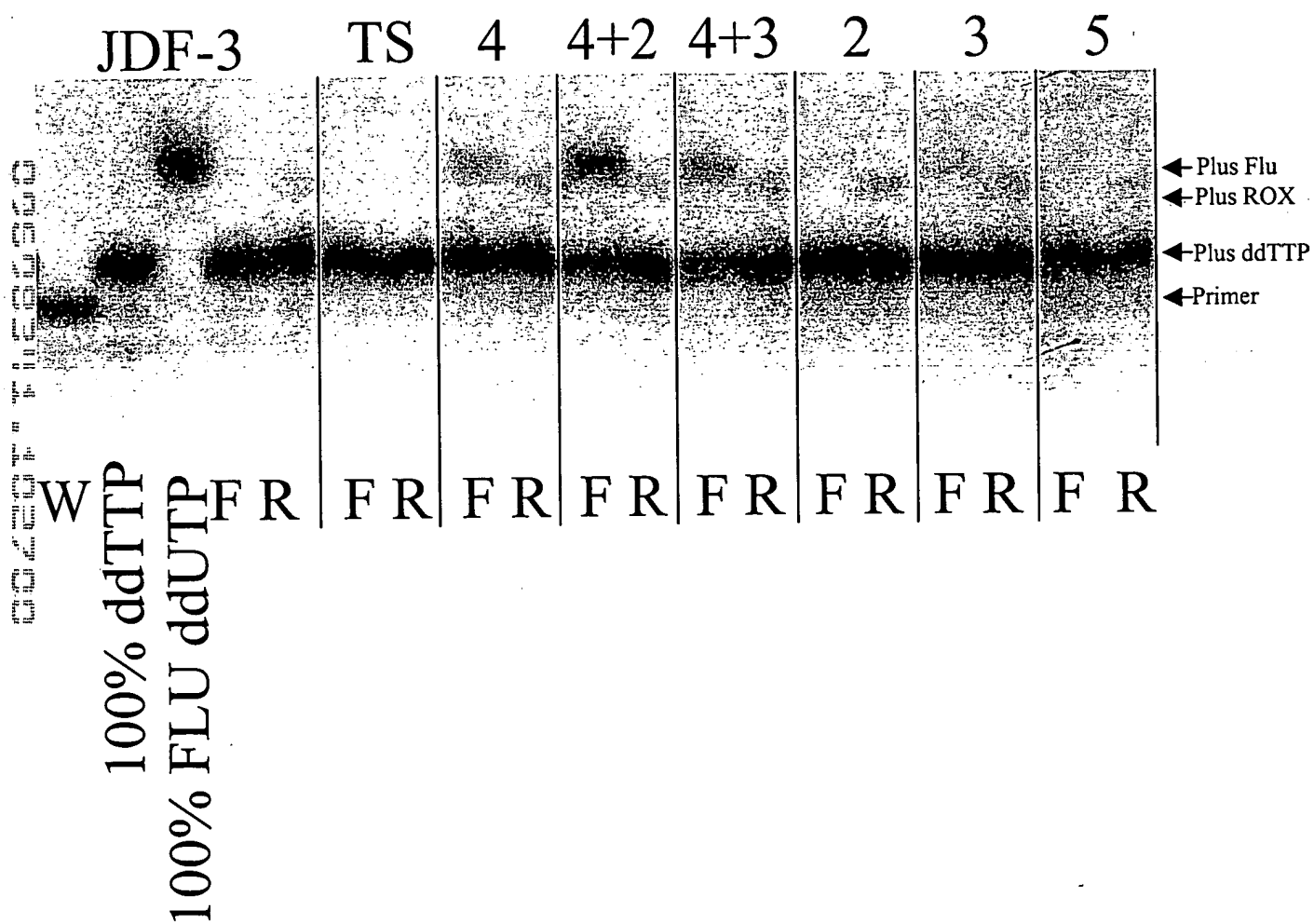


Figure 12

Flu ddUTP signal/ddTTP signal

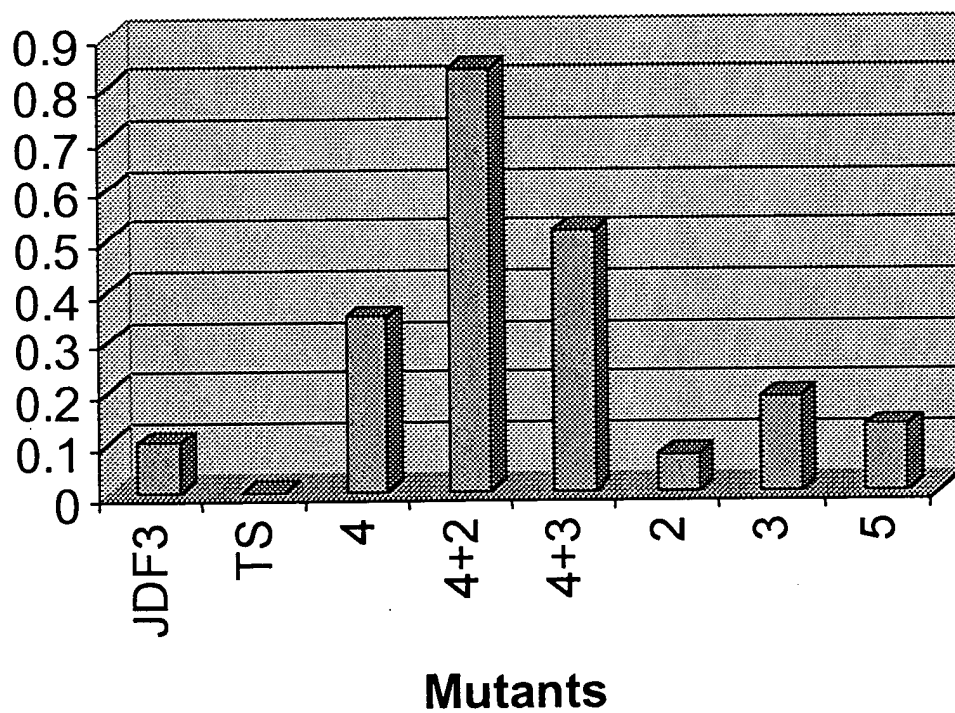


Figure 13



4	1	-----LVXNAXSTGNLVEWFLLRK
10	1	-----VWDVSRSTGNLVEWFLLRK
13	1	-----VWDVSRSTGNLVEWFLLRK
16	1	-----VWDVSRSTGNLVEWFLLRK
18	1	-----VWDVSRSTGNLVEWFLLRK
19	1	-----VWDVSRSTGNLVEWFLLRK
28	1	-----VWDVSRSTGNLVEWFLLRK
34	1	-----VWDVSRSTGNLVEWFLLRK
41	1	-----VWDVSRSTGNLVEWFLLRK
33	1	-----VWDVSRSTGNLVEWFLLRK
48	1	-----YWSXPXLRTGNLVEWFLLRK
55	1	-----VIGTXPRSTGNLVEWFLLRK
64	1	-----XXXFWDSRSTGNLVEWFLLRK
Jdf3	301	TGEGLERVARYSMEDARVTYELGREFFPMEAQLSRLIGQGVWDVSRSTGNLVEWFLLRK

4	20	AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
10	21	AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
13	21	AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
16	21	AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
18	21	AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
19	21	AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
28	21	AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
34	21	AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
41	21	AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
33	21	AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
48	21	AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
55	22	AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
64	24	AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
Jdf3	361	AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP

4	80	DTLNREGCRSYDVAPEVGHKFKCDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD
10	81	DTLNREGCRSYDVAPEVGHKFKCDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD
13	81	DTLNREGCRSYDVAPEVGHKFKCDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD
16	81	DTLNREGCRSYDVAPEVGHKFKCDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD
18	81	DTLNREGCRSYDVAPEVGHKFKCDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD
19	81	DTLNREGCRSYDVAPEVGHKFKCDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD
28	81	DTLNREGCRSYDVAPEVGHKFKCDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD
34	81	DTLNREGCRSYDVAPEVGHKFKCDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD
41	81	DTLNREGCRSYDVAPEVGHKFKCDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD
33	81	DTLNREGCRSYDVAPEVGHKFKCDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD
48	81	DTLNREGCRSYDVAPEVGHKFKCDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD
55	82	DTLNREGCRSYDVAPEVGHKFKCDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD
64	84	DTLNREGCRSYDVAPEVGHKFKCDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD
Jdf3	421	DTLNREGCRSYDVAPEVGHKFKCDFPGFIPSLLGNNLEERQKIKRKMKATLDPLEKNLLD

Figure 14

4 140 YRQRAIKILANSYYGYG<sup>1</sup>GYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 10 141 YRQRAIKILANSYYGYG<sup>2</sup>GYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 13 141 YRQRAIKILANSYYGYG<sup>3</sup>GYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 16 141 YRQRAIKILANSYYGYG<sup>4</sup>GYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 18 141 YRQRAIKILAN<sup>5</sup>YYGYG<sup>6</sup>GYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 19 141 YRQRAIKILANSYYGYG<sup>7</sup>GYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 28 141 YRQRAIKILANSYYGYG<sup>8</sup>GYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 34 141 YRQRAIKILANSYYGYG<sup>9</sup>GYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 41 141 YRQRAIKILANSYYGYG<sup>10</sup>GYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 33 141 YRQRAIKILANSYYGYG<sup>11</sup>GYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 48 141 YRQRAIKILANSYYGYG<sup>12</sup>GYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 55 142 YRQRAIKILANSYYGYG<sup>13</sup>GYARARW<sup>14</sup>YCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 64 144 YRQRAIKILANSYYG<sup>15</sup>NYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD  
 Jdf3 481 YRQRAIKILANSYYGYG<sup>16</sup>GYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD

4 200 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
 10 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
 13 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
 16 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLE<sup>1</sup>LEYEGFYVRGFFVTKKKYAVIDEE  
 18 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
 19 201 TDGLHATIPGADAETVKKKAMEFLNYIN<sup>2</sup>PKLPGLLELEYEGFYVRGFFVTKKK<sup>3</sup>YAVIDEE  
 28 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
 34 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
 41 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
 33 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLE<sup>4</sup>LEYEGFYVRGFFVTKKKYAVIDEE  
 48 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
 55 202 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
 64 204 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE  
 Jdf3 541 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE

4 260 GKITTRGLEIVRRDWSEIAKETQARVLEA<sup>1</sup>ILRHGDVEEAVRIVREVTEKLSKYEVPPEKL  
 10 261 GKITTRGLEIVRRDWSEIAKETQARVLEA<sup>2</sup>ILRHGDVEEAVRIVREVTEKLSKYEVPPE<sup>3</sup>KL  
 13 261 GKITTRGLEIVRRDWSEIAKETQARVLEA<sup>4</sup>ILRHGDVEEAVRIVR<sup>5</sup>TEKLSKYEVPPEKL  
 16 261 GKITTRGLEIVRRDWSEIAKETQARVLEA<sup>6</sup>ILRHGDVEEAVRIVREVTEKLSKYEVPPEKL  
 18 261 GKITTRGLEIVRRDWSEIAKETQARVLEA<sup>7</sup>ILRH<sup>8</sup>GDVEEAVRIVREVTEKLSKYEVPPEKL  
 19 261 GKITTRGLEIVRRDWS<sup>9</sup>KI<sup>10</sup>AKETQARVLEA<sup>11</sup>ILRHGDVEEA<sup>12</sup>VRIVREVTEKLSKYEVPPEKL  
 28 261 GK<sup>13</sup>I<sup>14</sup>TRGLEIVRRDWSEIAKETQARVLEA<sup>15</sup>ILRHGDVEEAVRIVREVTEKLSKYEVPPEKL  
 34 261 GKITTRGLEIVRRDWSEIAKETQARVLEA<sup>16</sup>ILRHGDVEEAVRIVREVTEKL<sup>17</sup>NKYEVPPEKL  
 41 261 GKITTRGLEIVRRDWSEIAKETQARVLEA<sup>18</sup>ILRHGDVEEAVRIVREVTEKLSKYEVPPEKL  
 33 261 GKITTRGLEIVRRDWSEIAKETQARVLEA<sup>19</sup>ILRHGDVEEAVRIVREVTEKLSKYEVPPEKL  
 48 261 GKITTRGLEIVRRDWSEIAKETQARVLEA<sup>20</sup>ILRHGDVEEAVRIVREVTEKLSKYEVP<sup>21</sup>PKL  
 55 262 GKITTRGLEIVRRDWSEIAKETQARVLEA<sup>22</sup>ILRHGDVEEAVRIVREVTEKLSKYEVP<sup>23</sup>PPGEA  
 64 264 GKITTRGLEIVRRDWSEIAKETQARVLEA<sup>24</sup>ILRHGDVEEAVRIVREVTEKLSKYEVPPEKL  
 Jdf3 601 GKITTRGLEIVRRDWSEIAKETQARVLEA<sup>25</sup>ILRHGDVEEAVRIVREVTEKLSKYEVPPEKL

Figure 15